SEQUENCE LISTING

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ggt ccc ctg ctt gcc cgg gac cgg aga cag gcc acc gaa tat gag tac   203
Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
        35                  40                  45

cta gat tat gat ttc ctg cca gaa acg gag cct cca gaa atg ctg agg   251
Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
    50                  55                  60

aac agc act gac acc act cct ctg act ggg cct gga acc cct gag tct   299
Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65                  70                  75                  80

acc act gtg gag cct gct gca agg cgt tct act ggc ctg gat gca gga   347
Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
                85                  90                  95

ggg gca gtc aca gag ctg acc acg gag ctg gcc aac atg ggg aac ctg   395
Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
            100                 105                 110

tcc acg gat tca gca gct atg gag ata cag acc act caa cca gca gcc   443
Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
        115                 120                 125

acg gag gca cag acc act cca ctg gca gcc aca gag gca cag aca act   491
Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr
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cga ctg acg gcc acg gag gca cag acc act cca ctg gca gcc aca gag   539
Arg Leu Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu
145                 150                 155                 160

gca cag acc act cca cca gca gcc acg gaa gca cag acc act caa ccc   587
Ala Gln Thr Thr Pro Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro
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aca ggc ctg gag gca cag acc act gca cca gca gcc atg gag gca cag   635
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acc act gca cca gca gcc atg gaa gca cag acc act cca cca gca gcc   683
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Ser Ala Thr Glu Ala Leu Ser Met Glu Pro Thr Thr Lys Arg Gly Leu
            260                 265                 270

ttc ata ccc ttt tct gtg tcc tct gtt act cac aag ggc att ccc atg   923
Phe Ile Pro Phe Ser Val Ser Ser Val Thr His Lys Gly Ile Pro Met
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gca gcc agc aat ttg tcc gtc aac tac cca gtg ggg gcc cca gac cac   971
Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
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atc tct gtg aag cag tgc ctg ctg gcc atc cta atc ttg gcg ctg gtg   1019
Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
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gcc act atc ttc ttc gtg tgc act gtg gtg ctg gcg gtc cgc ctc tcc   1067
Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
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cgc aag ggc cac atg tac ccc gtg cgt aat tac tcc ccc acc gag atg   1115
Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
            340                 345                 350

gtc tgc atc tca tcc ctg ttg cct gat ggg ggt gag ggg ccc tct gcc   1163
Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
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aca gcc aat ggg ggc ctg tcc aag gcc aag agc ccg ggc ctg acg cca   1211
Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
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gag ccc agg gag gac cgt gag ggg gat gac ctc acc ctg cac agc ttc   1259
Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu Thr Leu His Ser Phe
385                 390                 395                 400

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Leu Pro

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Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
         35                  40                  45

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
     50                  55                  60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 65                  70                  75                  80

Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
                 85                  90                  95

Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
            100                 105                 110

Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
        115                 120                 125

Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr
    130                 135                 140

Arg Leu Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu
145                 150                 155                 160

Ala Gln Thr Thr Pro Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro
                165                 170                 175

Thr Gly Leu Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala Gln
            180                 185                 190

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Pro Pro Ala Ala
        195                 200                 205

Met Glu Ala Gln Thr Thr Gln Thr Thr Ala Met Glu Ala Gln Thr Thr
    210                 215                 220

Ala Pro Glu Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu
225                 230                 235                 240

Ala Gln Thr Thr Pro Leu Ala Ala Met Glu Ala Leu Ser Thr Glu Pro
                245                 250                 255

Ser Ala Thr Glu Ala Leu Ser Met Glu Pro Thr Thr Lys Arg Gly Leu
            260                 265                 270
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Phe Ile Pro Phe Ser Val Ser Ser Val Thr His Lys Gly Ile Pro Met
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Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
    290                 295                 300

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305                 310                 315                 320

Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
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Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
            340                 345                 350

Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
        355                 360                 365

Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
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agc ttg cag ctg tgg gac acc tgg gca gat gaa gcc gag aaa gcc ttg   96
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
            20                  25                  30

ggt ccc ctg ctt gcc cgg gac cgg aga cag gcc acc gaa tat gag tac   144
Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
        35                  40                  45

cta gat tat gat ttc ctg cca gaa acg gag cct cca gaa atg ctg agg   192
Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
    50                  55                  60

aac agc act gac acc act cct ctg act ggg cct gga acc cct gag tct   240
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65                  70                  75                  80
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acc act gtg gag cct gct gca agg cgt tct act ggc ctg gat gca gga   288
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ggg gca gtc aca gag ctg acc acg gag ctg gcc aac atg ggg aac ctg   336
Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
            100                 105                 110

tcc acg gat tca gca gct atg gag ata cag acc act caa cca gca gcc   384
Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
        115                 120                 125

acg gag gca cag acc act caa cca gtg ccc acg gag gca cag acc act   432
Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
    130                 135                 140

cca ctg gca gcc aca gag gca cag aca act cga ctg acg gcc acg gag   480
Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
145                 150                 155                 160

gca cag acc act cca ctg gca gcc aca gag gca cag acc act cca cca   528
Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
                165                 170                 175

gca gcc acg gaa gca cag acc act caa ccc aca ggc ctg gag gca cag   576
Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
            180                 185                 190

acc act gca cca gca gcc atg gag gca cag acc act gca cca gca gcc   624
Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
        195                 200                 205

atg gaa gca cag acc act cca cca gca gcc atg gag gca cag acc act   672
Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
    210                 215                 220

caa acc aca gcc atg gag gca cag acc act gca cca gaa gcc acg gag   720
Gln Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu
225                 230                 235                 240

gca cag acc act caa ccc aca gcc acg gag gca cag acc act cca ctg   768
Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu
                245                 250                 255

gca gcc atg gag gcc ctg tcc aca gaa ccc agt gcc aca gag gcc ctg   816
Ala Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu
            260                 265                 270

tcc atg gaa cct act acc aaa aga ggt ctg ttc ata ccc ttt tct gtg   864
Ser Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val
        275                 280                 285

tcc tct gtt act cac aag ggc att ccc atg gca gcc agc aat ttg tcc   912
Ser Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser
    290                 295                 300
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gtc aac tac cca gtg ggg gcc cca gac cac atc tct gtg aag cag tgc   960
Val Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
305                 310                 315                 320

ctg ctg gcc atc cta atc ttg gcg ctg gtg gcc act atc ttc ttc gtg   1008
Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
                325                 330                 335

tgc act gtg gtg ctg gcg gtc cgc ctc tcc cgc aag ggc cac atg tac   1056
Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr
            340                 345                 350

ccc gtg cgt aat tac tcc ccc acc gag atg gtc tgc atc tca tcc ctg   1104
Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu
        355                 360                 365

ttg cct gat ggg ggt gag ggg ccc tct gcc aca gcc aat ggg ggc ctg   1152
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    370                 375                 380

tcc aag gcc aag agc ccg ggc ctg acg cca gag ccc agg gag gac cgt   1200
Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg
385                 390                 395                 400

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Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
         35                  40                  45

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
     50                  55                  60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 65                  70                  75                  80

Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
                 85                  90                  95

Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
            100                 105                 110

Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
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Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
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Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
                165                 170                 175

Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
            180                 185                 190

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
        195                 200                 205

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
    210                 215                 220

Gln Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu
225                 230                 235                 240

Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu
                245                 250                 255

Ala Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu
            260                 265                 270

Ser Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val
        275                 280                 285

Ser Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser
    290                 295                 300

Val Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
305                 310                 315                 320

Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
                325                 330                 335

Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr
            340                 345                 350

Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu
        355                 360                 365

Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu
    370                 375                 380

Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg
385                 390                 395                 400

Glu Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
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<210> 13
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13
aattctagca ctgcttcaca gagatgtggt ctggtgctcc cactgggtag tt 52

<210> 14
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
aactacccag tgggagcacc agaccacatc tctgtgaagc agtag 45

<210> 15
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
aattctactg cttcacagag atgtggtctg gtgctcccac tgggtagtt 49

<210> 16
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 16
ctagacccgg gatggcatcc atgacaggag gacaacaaat ggtaggccgt ag 52

<210> 17
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 17
aattctacgg cctacccatt tgttgtcctc ctgtcatgga tgccatcccg ggt 53

<210> 18
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18
ctgcggccgc agt 13

<210> 19
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19
ctagactgcg gccgcag 17

<210> 20
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20
ccaggtccaa ctgcaggtcg actctagagg gcacttcttc tgggcccacg 50

<210> 21
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21
tattatctgt gcggccgccc tccagaaccc atggctgctg gttgcagtgg 50

<210> 22
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 22
tattatctgt gcggccgcgc agcaggctcc acagtggtag 40

<210> 23
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 23
tattatctgt gcggccgcgg aggctccgtt tctggcag 38

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
cggagacagg ccaccgaatt cctgccagaa acg 33

<210> 25
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
cctccagaaa tgctgaggca cagcactgac accactcctc 40

<210> 26
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
gagctggcca acatggggca actgtccacg gattcagcag 40

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
aattcgagtt cctagatttt g 21

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 28
aattcaaaat ctaggaactc g 21

<210> 29
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 29
aattcgagta cctagattat gatttcctgc cagaaactga gcctccgc 48

<210> 30
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 30
ggccgcggag gctcagtttc tggcaggaaa tcataatcta ggtactcg 48

<210> 31
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 31
aattcgagtt cctagattat gatttcctgc cagaaactga gcctccgc 48

<210> 32
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 32
ggccgcggag gctcagtttc tggcaggaaa tcataatcta ggaactcg 48

<210> 33
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 33
aattcgagtt cctagatttc gatttcctgc cagaaactga gcctccgc 48

<210> 34
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 34
ggccgcggag gctcagtttc tggcaggaaa tcgaaatcta ggaactcg 48

<210> 35
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 35
atgcctctgc aactcctcct gttgctgatc ctactgggcc ctggcaacag cttgcagctg 60
tgggacacct gggcagatga agccgagaaa gccttgggtc ccctgcttgc ccgggaccgg 120
agacaggcca ccgaatatga gtacctagat tatgatttcc tgccagaaac ggagcctcca 180
gaaatgctga ggaacagcac tgacaccact cctctgactg ggcctggaac ccctgagtct 240
accactgtgg agcctgctgc gcggccgcac acatgcccac cgtgcccagc acctgaagcc 300
ctgggggcac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 360
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 420
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 480
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 540
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagtccc catcgagaaa 600
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 660
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 720
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 780
cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 840
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 900
cactacacgc agaagagcct ctccctgtcc ccgggtaaat ga 942

<210> 36
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
fusion protein

<400> 36
Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
1 5 10 15

Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
20 25 30

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
35 40 45

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
50 55 60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65 70 75 80

Thr Thr Val Glu Pro Ala Ala Arg Pro His Thr Cys Pro Pro Cys Pro
85 90 95

Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
100 105 110

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
115 120 125

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
130 135 140

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
145 150 155 160

```
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                165                 170                 175

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            180                 185                 190

Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        195                 200                 205

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    210                 215                 220

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
225                 230                 235                 240

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                245                 250                 255

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            260                 265                 270

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        275                 280                 285

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    290                 295                 300

Lys Ser Leu Ser Leu Ser Pro Gly Lys
305                 310
```

<210> 37
<211> 810
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 37

```
atgcctctgc aactcctcct gttgctgatc ctactgggcc ctggcaacag cttgcagctg 60
tgggacacct gggcagatga agccgagaaa gccttgggtc ccctgcttgc ccgggaccgg 120
agacaggcca ccgaatatga gtacctagat tatgatttcc tgccagaaac ggagcctcca 180
gaaatgctga ggaacagcac tgacaccact cctctgactg ggcctggaac ccctgagtct 240
accactgtgg agcctgctgc gcggccgctg tgtgccaacc tagtaccggt gcccatcacc 300
aacgccaccc tggaccagat cactggcaag tggttttata tcgcatcggc ctttcgaaac 360
gaggagtaca ataagtcggt tcaggagatc caagcaacct tcttttactt caccccaac 420
aagacagagg acacgatctt tctcagagag taccagaccc gacaggacca gtgcatctat 480
aacaccacct acctgaatgt ccagcgggaa aatgggacca tctccagata cgtgggaggc 540
caagagcatt tcgctcactt gctgatcctc agggacacca agacctacat gcttgctttt 600
gacgtgaacg atgagaagaa ctgggggctg tctgtctatg ctgacaagcc agagacgacc 660
aaggagcaac tgggagagtt ctacgaagct ctcgactgct tgcgcattcc caagtcagat 720
gtcgtgtaca ccgattggaa aaaggataag tgtgagccac tggagaagca gcacgagaag 780
gagaggaaac aggaggaggg ggaatcctag                                  810
```

<210> 38
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic fusion protein

<400> 38

```
Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
  1               5                  10                  15

Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
             20                  25                  30

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
         35                  40                  45

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
     50                  55                  60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 65                  70                  75                  80

Thr Thr Val Glu Pro Ala Ala Arg Pro Leu Cys Ala Asn Leu Val Pro
                 85                  90                  95

Val Pro Ile Thr Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe
            100                 105                 110

Tyr Ile Ala Ser Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln
        115                 120                 125

Glu Ile Gln Ala Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp
    130                 135                 140

Thr Ile Phe Leu Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr
145                 150                 155                 160

Asn Thr Thr Tyr Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg
                165                 170                 175

Tyr Val Gly Gly Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp
            180                 185                 190

Thr Lys Thr Tyr Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp
        195                 200                 205

Gly Leu Ser Val Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu
    210                 215                 220

Gly Glu Phe Tyr Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp
225                 230                 235                 240

Val Val Tyr Thr Asp Trp Lys Lys Asp Lys Cys Glu Pro Leu Glu Lys
                245                 250                 255
```

Gln His Glu Lys Glu Arg Lys Gln Glu Glu Gly Glu Ser
260 265

<210> 39
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 39
atggtggccg ggacccgctg tcttctagcg ttgctgcttc cccaggtcct cctgggcggc 60
gcggctggcc tcgttccgga gctgggccgc aggaagttcg cggcggcgtc gtcgggccgc 120
ccctcatccc agccctctga cgaggtcctg agcgagttcg agttgcggct gctcagcatg 180
ttcggcctga aacagagacc cacccccagc agggacgccg tggtgccccc ctacatgcta 240
gacctgtatc gcaggcactc aggtcagccg ggctcacccg ccccagacca ccggttggag 300
agggcagcca gccgagccaa cactgtgcgc agcttccacc atgaagaatc tttggaagaa 360
ctaccagaaa cgagtgggaa aacaacccgg agattcttct ttaatttaag ttctatcccc 420
acggaggagt ttatcacctc agcagagctt caggttttcc gagaacagat gcaagatgct 480
ttaggaaaca atagcagttt ccatcaccga attaatattt atgaaatcat aaaacctgca 540
acagccaact cgaaattccc cgtgaccaga cttttggaca ccaggttggt gaatcagaat 600
gcaagcaggt gggaaagttt tgatgtcacc cccgctgtga tgcggtggac tgcacaggga 660
cacgccaacc atggattcgt ggtggaagtg gcccacttgg aggagaaaca aggtgtctcc 720
aagagacatg ttaggataag caggtctttg caccaagatg aacacagctg gtcacagata 780
aggccattgc tagtaacttt tggccatgat ggaaaagggc atcctctcca caaaagagaa 840
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cctttgtacg tggacttcag tgacgtgggg tggaatgact ggattgtggc tcccccgggg 1080
tatcacgcct tttactgcca cggagaatgc ccttttcctc tggctgatca tctgaactcc 1140
actaatcatg ccattgttca gacgttggtc aactctgtta actctaagat tcctaaggca 1200
tgctgtgtcc cgacagaact cagtgctatc tcgatgctgt accttgacga gaatgaaaag 1260
gttgtattaa agaactatca ggacatggtt gtggagggtt gtgggtgtcg ctag 1314

<210> 40
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic fusion protein

<400> 40
Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
1 5 10 15

Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
20 25 30

Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
35 40 45

```
Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
     50                  55                  60

Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
 65                  70                  75                  80

Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
                 85                  90                  95

His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
            100                 105                 110

His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
        115                 120                 125

Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
    130                 135                 140

Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
145                 150                 155                 160

Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
                165                 170                 175

Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
            180                 185                 190

Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
        195                 200                 205

Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
    210                 215                 220

Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
225                 230                 235                 240

Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
                245                 250                 255

Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
            260                 265                 270

Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Thr Glu Tyr Glu
        275                 280                 285

Tyr Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu
    290                 295                 300

Arg Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu
305                 310                 315                 320

Ser Thr Thr Val Glu Pro Ala Ala Arg Arg Lys Arg Leu Lys Ser Ser
                325                 330                 335

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
            340                 345                 350
```

```
Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
        355                 360                 365

Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
    370                 375                 380

Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
385                 390                 395                 400

Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
                405                 410                 415

Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
            420                 425                 430

Gly Cys Gly Cys Arg
        435
```

<210> 41
<211> 795
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 41
atgcctctgc aactcctcct gttgctgatc ctactgggcc ctggcaacag cttgcagctg 60
tgggacacct gggcagatga agccgagaaa gccttgggtc ccctgcttgc ccgggaccgg 120
agacaggcca ccgaatatga gtacctagat tatgatttcc tgccagaaac ggagcctcca 180
gaaatgctga ggaacagcac tgacaccact cctctgactg ggcctggaac ccctgagtct 240
accactgtgg agcctgctgc gcggccgcca cctggccccc ctcgagtttc cccagaccct 300
cgggccgagc tggacagcac cgtgctcctg acccgctctc tcctggcgga cacgcggcag 360
ctggctgcac agctgaggga caaattccca gctgacgggg accacaacct ggattccctg 420
cccaccctgg ccatgagtgc gggggcactg ggagctctac agctcccagg tgtgctgaca 480
aggctgcgag cggacctact gtcctacctg cggcacgtgc agtggctgcg ccgggcaggt 540
ggctcttccc tgaagaccct ggagcccgag ctgggcaccc tgcaggcccg actggaccgg 600
ctgctgcgcc ggctgcagct cctgatgtcc cgcctggccc tgccccagcc acccccggac 660
ccgccggcgc ccccgctggc gccccctcc tcagcctggg ggggcatcag ggccgcccac 720
gccatcctgg gggggctgca cctgacactt gactgggccg tgaggggact gctgctgctg 780
aagactcggc tgtga 795

<210> 42
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic fusion protein

<400> 42
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Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
  1               5                  10                  15
```

```
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
            20                  25                  30

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
        35                  40                  45

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
    50                  55                  60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65                  70                  75                  80

Thr Thr Val Glu Pro Ala Ala Arg Pro Pro Pro Gly Pro Pro Arg Val
                85                  90                  95

Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr Arg
            100                 105                 110

Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp Lys
        115                 120                 125

Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu Ala
    130                 135                 140

Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu Thr
145                 150                 155                 160

Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp Leu
                165                 170                 175

Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu Gly
            180                 185                 190

Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu Leu
        195                 200                 205

Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala Pro
    210                 215                 220

Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala His
225                 230                 235                 240

Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg Gly
                245                 250                 255

Leu Leu Leu Leu Lys Thr Arg Leu
            260
```

<210> 43
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 43
Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe Leu Pro Glu Cys
1 5 10 15

<210> 44
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 44
Ser Tyr Leu Asp Tyr Ser
1 5

<210> 45
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 45
Ser Phe Leu Asp Tyr Ser
1 5

<210> 46
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 46
Arg Asp Arg Arg
1

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid consensus sequence

<220>
<221> MOD_RES
<222> (2)
<223> Thr or Met

<220>
<221> MOD_RES
<222> (8)
<223> Pro, Ala, Gln, Glu, or Arg

<220>
<221> MOD_RES
<222> (9)
<223> Pro or Leu

<220>
<221> MOD_RES
<222> (10)
<223> Ala or Thr

<400> 47
Ala Xaa Glu Ala Gln Thr Thr Xaa Xaa Xaa
1 5 10

<210> 48
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 48
Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe Leu Pro Glu Thr
1 5 10 15

Glu Pro Pro Glu Met Leu Arg Asn Ser Thr Asp Thr Thr Pro Thr
20 25 30